

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 10:42:32 ; Search time 164 Seconds  
(without alignments)

23.583 Million cell updates/sec

Title: US-09-147-490-1

Perfect score: 58

Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	2	AAR97348 Peptide f
2	58	100.0	10	2	Aaw30318 Peptide h
3	58	100.0	10	2	Aaw37247 Angiotens
4	58	100.0	10	4	Aau79893 Anti-stre
5	58	100.0	10	5	ABG31639 Hemorhin
6	58	100.0	10	6	ABP72839 Angiotens
7	58	100.0	12	6	AAO30111 Human bet
8	58	100.0	74	1	AAP50291 Sequence
9	58	100.0	74	2	AAR69602 Human bet
10	58	100.0	86	4	AAO07245 Human pol
11	58	100.0	104	4	AAU30074 Novel hum
12	58	100.0	110	4	AAO02538 Human pol
13	58	100.0	112	2	AAR89261 Human bet
14	58	100.0	112	2	AAR89262 Human bet
15	58	100.0	121	3	AAO01752 Human sec
16	58	100.0	124	4	AAU29698 Novel hum
17	58	100.0	127	4	AAO13066 Human pol
18	58	100.0	128	4	AAO09585 Human pol
19	58	100.0	130	6	ABR82319 Human met
20	58	100.0	137	4	AAU30769 Novel hum
21	58	100.0	140	4	AAU79250 Human pro
22	58	100.0	140	5	ABP63040 Human pol
23	58	100.0	141	2	AAW30718 Haemoglob
24	58	100.0	142	4	AAU29784 Novel hum
25	58	100.0	143	4	AAU30030 Novel hum

26	58	100.0	143	4	AAU30028	Novel hum
27	58	100.0	143	4	AAU29890	Novel hum
28	58	100.0	143	4	AAU29961	Novel hum
29	58	100.0	143	4	AAU30083	Novel hum
30	58	100.0	143	4	AAU29796	Novel hum
31	58	100.0	143	4	AAU32926	Novel hum
32	58	100.0	143	4	AAU29847	Novel hum
33	58	100.0	143	4	AAU29929	Novel hum
34	58	100.0	143	4	AAU30022	Novel hum
35	58	100.0	143	4	AAU30132	Novel hum
36	58	100.0	143	4	AAU29798	Novel hum
37	58	100.0	143	4	AAU29977	Novel hum
38	58	100.0	143	4	AAU29855	Novel hum
39	58	100.0	143	4	AAU30020	Novel hum
40	58	100.0	143	4	AAU30024	Novel hum
41	58	100.0	143	4	AAU30099	Novel hum
42	58	100.0	143	4	AAU29920	Novel hum
43	58	100.0	144	2	AAR29611	Mutant hu
44	58	100.0	144	2	AAR39726	HbA McKee
45	58	100.0	144	2	AAW73382	Human hae

#### ALIGNMENTS

##### RESULT 1

AAR97348

ID AAR97348 standard; protein; 10 AA.

XX

AC AAR97348;

XX

DT 17-OCT-1996 (first entry)

XX

DE Peptide fragment of haemoglobin B (Haemorphin 10).

XX

KW haemoglobin; INPROL; stem cell proliferation; B lymphocytes; B cells;

KW chemotherapy; cancer; haematopoietic cells; marrow; blood; vaccination;

KW myeloproliferative disease; autoimmune disease; adjuvant; gene therapy.

XX

OS Homo sapiens.

XX

PN WO9610634-A1.

XX

PD 11-APR-1996.

XX

PF 29-SEP-1995; 95WO-US012268.

XX

PR 30-SEP-1994; 94US-00316424.

XX

PR 28-SEP-1995; 95US-00535882.

XX

PA (PRON-) PRO-NEURON INC.

XX

PI Kozlov V, Tsyrova I, Wolpe SD;

XX

DR WPI; 1996-209356/21.

XX

PT Inhibitors of stem cell proliferation comprising haemoglobin chains -

PT useful in mammals, e.g. for protecting stem cells from antiviral agents,

XX

PT treating cancer, and maintaining mammalian haematopoietic stem cells ex

XX

PS Claim 17; Page 65; 101pp; English.

XX

CC Compositions (INPROL) comprising a polypeptide selected from the

CC haemoglobin alpha, beta, gamma, delta, epsilon or zeta chains and a

CC carrier may be used to inhibit stem cell proliferation. INPROL can also

CC be used for stimulating the growth of B cells and can be used with ratio-

CC or chemotherapy to treat cancer in mammals by differentially protecting

CC normal stem cells and not cancer cells from such therapy. INPROL is also

CC useful for maintaining mammalian haematopoietic stem cells ex vivo

CC (particularly bone marrow, peripheral blood or cord blood cells); for the

CC ex vivo expansion of haematopoietic cells when used in combination with a

CC stimulatory cytokine. INPROL can also be used to treat myeloproliferative  
 CC or autoimmune disease. INPROL is also useful as an adjuvant in the  
 CC vaccination of mammals and can be used to treat a mammal with  
 CC immunodepression caused by stem cell proliferation. INPROL can also be  
 CC used in gene therapy. This peptide fragment of human haemoglobin B  
 CC corresponds to amino acids 32-41 of the mature protein given in AAR97358  
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
 |||||  
 Db 1 LVVYPWTQRF 10

RESULT 2  
 AAW30318  
 ID AAW30318 standard; peptide; 10 AA.

XX

AC AAW30318;

XX 20-APR-1998 (first entry)

XX Peptide haemorphin 10 with opiate activity.

XX INPROL; stem cell; inhibition; stimulation; proliferation; myoglobin;  
 KW alpha chain; haemoglobin; radiotherapy; chemotherapy; cancer;  
 KW differential protection; stem cell hypoproliferation; aplastic anaemia;  
 KW stem cell exhaustion; haemorphin; opiate activity.

XX Synthetic.

OS Homo sapiens.

XX WO9736922-A1.

XX 09-OCT-1997.

XX 03-APR-1997; 97WO-US005601.

XX 03-APR-1996; 96US-00627173.

XX (PRON-) PRO-NEURON INC.

XX Wolpe SD, Tsyrlava I;

XX WPI; 1997-503044/46.

XX Haemoglobin alpha chain derivatives - used to inhibit or stimulate stem  
 PT cell proliferation, for treatment of cancer, immune depression etc.

XX Claim 49; Page 117; 162pp; English.

XX The present peptide is derived from amino acids 32-41 of the beta chain  
 CC of adult human haemoglobin. The peptide has sequence similarity and  
 CC biological activity similar to other atypical opiate peptides. The  
 CC peptide can stimulate or inhibit stem cell proliferation, similar to  
 CC INPROL compounds. The peptide is used to inhibit stem cell proliferation,  
 CC particularly during radiotherapy or chemotherapy of cancer, but more  
 CC generally wherever a mammal is exposed to an agent, e.g. an antiviral,  
 CC that damages or destroys stem cells. It can also be used for differential  
 CC protection of normal stem cells, but not cancer cells, from chemotherapy  
 CC or radiation, particularly after normal stem cells have been induced to  
 CC proliferate by therapeutic treatment. The peptide can also be used for  
 CC control of stem cell hypoproliferation (e.g. aplastic anaemia), for  
 CC treating or preventing stem cell exhaustion (e.g. where caused by  
 CC acquired immune deficiency syndrome), and to treat or prevent  
 CC immunodeficiency. INPROL can also be used for treating pain in a mammal.  
 CC INPROL and related compounds reversibly inhibit or stimulate stem cells  
 CC depending on the dose, so allow precise control over cycling of these  
 CC cells

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
 |||||  
 Db 1 LVVYPWTQRF 10

RESULT 3  
 AAW37247  
 ID AAW37247 standard; peptide; 10 AA.

XX

AC AAW37247;

XX 18-JUN-1998 (first entry)

XX Angiotensin IV activity exhibiting neuroactive peptide LVV-haemorphin-7.  
 KW Angiotensin IV; neuroactive; Alzheimer's disease; modulator; dementia;  
 KW neuronal development; vasoeffective; neuropathy; brain injury;  
 KW LVV-haemorphin-7.

XX Synthetic.

OS Macaca fascicularis.

XX WO9801465-A1.

XX 15-JAN-1998.

XX 09-JUL-1997; 97WO-AU000436.

XX 09-JUL-1996; 96AU-00008993.

XX (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.

XX Mendelsohn FAO, Chai SY, Moeller I, Aldred PG, Smith IA, Lew RA;

XX WPI; 1998-100995/09.

XX Neuro-active peptide with activities of angiotensin IV and related DNA -  
 PT antagonists and oligonucleotide(s), useful for modulating neuronal  
 PT development and activity of motor and cholinergic neurons.

XX Claim 1; Page 45; 65pp; English.

XX This LVV-haemorphin-7 is a neuroactive peptide with at least 1 of the  
 CC activities of angiotensin IV. This is an agonist of the angiotensin IV  
 CC receptor and is its endogenous ligand in the brain. It can modulate  
 CC learning or behaviour and has vasoactive effects and can dilate cerebral  
 CC arteries, increase renal blood flow and stereotypy behaviour, facilitate  
 CC memory retrieval, induce neurite remodelling, and alleviate effects of  
 CC spinal cord injuries. This peptide and its antagonists are used to  
 CC modulate activity of motor, cholinergic neurons and neuronal development.  
 CC Specific applications are in treatment of dementia, Alzheimer's disease,  
 CC neurodegeneration (involving cholinergic, motor or sensory pathways),  
 CC sensory and motor peripheral neuropathy, brain injury and spinal cord  
 CC injury (caused by one or more of trauma, hypoxia and/or vascular  
 CC disease). Antibodies specific for the peptide can be used to determine  
 CC its amount of in tissues and tissue regions

XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
 |||||  
 Db 1 LVVYPWTQRF 10

XX PF 31-JAN-2002; 2002WO-EP000978.  
 XX 02-FEB-2001; 2001EP-00102383.  
 PR 08-FEB-2001; 2001US-0267186P.  
 XX (SOLV ) SOLVAY PHARM GMBH.  
 XX Lammerich H, Busmann A, Kutzleb C, Wendland M, Seiler P;  
 PI Berger C, Eickelmann P, Meyer M, Forssmann W, Maronde E;  
 XX WPI; 2002-627570/67.  
 XX Determining if a substance is a potential ligand of a bombesin receptor  
 PT subtype 3 (BRS-3), useful for preparing a composition for treating e.g.  
 PT cancer, comprises contacting cell expressing the BRS-3 polypeptide with  
 PT hemorphin ligands.  
 XX Example 2; Page 12; 64pp; English.  
 XX The present invention relates to a new method of determining if a  
 CC substance is a potential ligand of a bombesin receptor subtype 3 (BRS-3)  
 CC polypeptide receptor. The method of the invention involves contacting  
 CC cells expressing the BRS-3 polypeptide receptor, or a receptor membrane  
 CC preparation comprising the BRS-3 polypeptide receptor, with labelled  
 CC hemorphin ligands VV-H-7 or LVV-H-7 in the presence and in the absence of  
 CC the substance, and measuring the binding of the ligand to the receptor.  
 CC The compound or the antagonist is useful for preparing a pharmaceutical  
 CC composition for the treatment and/or prophylaxis of BRS-3/hemorphin  
 CC ligand based dysfunctions, disorders or diseases that are related to cell  
 CC growth, cell proliferation, tumour development and cancer, preferably  
 CC small cell lung carcinoma (SCLC), neoplasm, immunology and inflammation,  
 CC or to genitourinary system, or to any other dysfunction, disorder or  
 CC disease related to the activities of BRS-3, in particular of hBRS-3, in  
 CC connection with its interrelation with VV-H-7 and/or LVV-H-7. The protein  
 CC -ligand complex is useful for the design and modulation or optimisation  
 CC of lead structures with BRS-3 polypeptide-binding activity. The validated  
 CC animal models are useful for evaluating identified agonists or  
 CC antagonists at BRS-3 polypeptide receptor in dysfunctions, disorders or  
 CC diseases. The BRS-3 polypeptide is useful in diagnosing the diseases  
 CC mentioned, or a subject's susceptibility to it, and in screening methods  
 CC for identifying the compound, antagonist or agonist. The present amino  
 CC acid sequence represents the hemorphin ligand LVV-H-7 peptide that was  
 CC used in the methods of the invention  
 XX Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 58; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVVYPWTQRF 10  
 DB 1 LVVYPWTQRF 10  
 RESULT 5  
 ABG31639  
 ID ABG31639 standard; peptide; 10 AA.  
 XX AC ABG31639;  
 XX 29-NOV-2002 (first entry)  
 XX Hemorphin ligand LVV-H-7 peptide.  
 XX Human; bombesin receptor subtype 3; BRS-3; receptor; hemorphin ligand;  
 KW VV-H-7; LVV-H-7; cell growth; cell proliferation; tumour development;  
 KW cancer; small cell lung carcinoma; SCLC; neoplasm; immunology;  
 KW inflammation; genitourinary system; cytostatic; antiinflammatory;  
 KW immunomodulator; bombesin agonist; bombesin antagonist; vaccine;  
 KW gene therapy.  
 XX Synthetic.  
 OS  
 XX WO200263305-A2.  
 PN  
 XX 15-AUG-2002.  
 PD

XX PF 31-JAN-2002; 2002WO-EP000978.  
 XX 02-FEB-2001; 2001EP-00102383.  
 PR 08-FEB-2001; 2001US-0267186P.  
 XX (SOLV ) SOLVAY PHARM GMBH.  
 XX Lammerich H, Busmann A, Kutzleb C, Wendland M, Seiler P;  
 PI Berger C, Eickelmann P, Meyer M, Forssmann W, Maronde E;  
 XX WPI; 2002-627570/67.  
 XX Determining if a substance is a potential ligand of a bombesin receptor  
 PT subtype 3 (BRS-3), useful for preparing a composition for treating e.g.  
 PT cancer, comprises contacting cell expressing the BRS-3 polypeptide with  
 PT hemorphin ligands.  
 XX Example 2; Page 12; 64pp; English.  
 XX The present invention relates to a new method of determining if a  
 CC substance is a potential ligand of a bombesin receptor subtype 3 (BRS-3)  
 CC polypeptide receptor. The method of the invention involves contacting  
 CC cells expressing the BRS-3 polypeptide receptor, or a receptor membrane  
 CC preparation comprising the BRS-3 polypeptide receptor, with labelled  
 CC hemorphin ligands VV-H-7 or LVV-H-7 in the presence and in the absence of  
 CC the substance, and measuring the binding of the ligand to the receptor.  
 CC The compound or the antagonist is useful for preparing a pharmaceutical  
 CC composition for the treatment and/or prophylaxis of BRS-3/hemorphin  
 CC ligand based dysfunctions, disorders or diseases that are related to cell  
 CC growth, cell proliferation, tumour development and cancer, preferably  
 CC small cell lung carcinoma (SCLC), neoplasm, immunology and inflammation,  
 CC or to genitourinary system, or to any other dysfunction, disorder or  
 CC disease related to the activities of BRS-3, in particular of hBRS-3, in  
 CC connection with its interrelation with VV-H-7 and/or LVV-H-7. The protein  
 CC -ligand complex is useful for the design and modulation or optimisation  
 CC of lead structures with BRS-3 polypeptide-binding activity. The validated  
 CC animal models are useful for evaluating identified agonists or  
 CC antagonists at BRS-3 polypeptide receptor in dysfunctions, disorders or  
 CC diseases. The BRS-3 polypeptide is useful in diagnosing the diseases  
 CC mentioned, or a subject's susceptibility to it, and in screening methods  
 CC for identifying the compound, antagonist or agonist. The present amino  
 CC acid sequence represents the hemorphin ligand LVV-H-7 peptide that was  
 CC used in the methods of the invention  
 XX Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 58; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVVYPWTQRF 10  
 DB 1 LVVYPWTQRF 10  
 RESULT 6  
 ABP72839  
 ID ABP72839 standard; peptide; 10 AA.  
 XX AC ABP72839;  
 XX 11-AUG-2003 (first entry)  
 XX Angiotensin IV receptor modulator peptide.  
 XX Angiotensin IV; receptor; insulin-regulated aminopeptidase; IRAP;  
 KW neurotropic; antiparkinsonian; vulnery; gynaeological; neuroprotective;  
 KW antiangiogenic; cytostatic; sheep; vaccine; gene therapy.  
 XX Ovies aries.  
 OS  
 XX WO2003011304-A1.  
 PN

XX PD 13-FEB-2003.  
 XX PF 02-AUG-2002; 2002WO-AU001034.  
 XX PR 02-AUG-2001; 2001AU-00006772.  
 XX PR 17-OCT-2001; 2001US-0330170P.  
 XX PA (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.  
 XX PI Albiston AL, McDowall SG, Mendelsohn FAO, Chai SY;  
 XX DR WPI; 2003-278368/27.  
 XX PT Modulating the expression, production or activity of AT4 receptor/insulin  
 PT -regulated aminopeptidase (IRAP) for preventing or treating e.g.,  
 PT Parkinson's disease, comprises administering a modulator of AT4  
 PT receptor/IRAP.  
 XX PS Claim 26; Page 102; 146pp; English.  
 XX CC The present sequence is that of a peptide isolated from the sheep  
 CC cerebral cortex. This decapeptide binds with nanomolar affinity to the  
 CC angiotensin IV (AT4) receptor and which mimics the actions of human AT4.  
 CC The AT4 receptor has been identified insulin-regulated aminopeptidase  
 CC (IRAP). The invention provides a method of screening for compounds which  
 CC can modulate the activity of the AT4 receptor/IRAP. The compound is: a  
 CC ligand of AT4 receptor/IRAP, such as the present decapeptide; an  
 CC oligonucleotide that is antisense to a nucleic acid encoding AT4  
 CC receptor/IRAP; or a compound that is able to modulate the cellular  
 CC localisation of AT4 receptor/IRAP. The compound can be used to: treat or  
 CC prevent a disorder of the central nervous system associated with dementia  
 CC and/or memory loss, motor and sensory systems, trauma or stroke, or a  
 CC disorder of the cardiovascular system, development and/or growth, glucose  
 CC and fat metabolism, reproductive tract, cancer or a disorder associated  
 CC with pregnancy, a neurodegenerative condition selected from motor neuron  
 CC disease (amyotrophic lateral sclerosis), progressive spinal muscular  
 CC atrophy, infantile muscular atrophy, Charcot-Marie-Tooth disease,  
 CC Parkinson's disease, Parkinson-Plus syndrome, Guamanian Parkinsonian  
 CC dementia complex, progressive bulbar atrophy and Alzheimer's disease, a  
 CC neurodegenerative condition arising from ischaemia, hypoxia, neural  
 CC injury, surgery or exposure to neurotoxins, a peripheral sensory  
 CC neuropathy resulting from exposure to drugs, toxins or to diabetes, a  
 CC condition characterised by neuronal deficit or neuronal death, and also  
 CC memory disorders and memory loss; enhance memory and/or learning; to  
 CC modulate in vivo uptake of glucose into cells or tissues; and to  
 CC stimulate growth in an animal, especially a farm animal (all claimed).  
 CC Note: The present sequence is identified as SEQ ID 2 in Claim 26, but is  
 CC SEQ ID 3 in the sequence listing  
 XX SQ Sequence 10 AA;  
 Query Match 100.0%; Score 58; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LVVYPWTQRF 10  
 Db 1 LVVYPWTQRF 10  
 RESULT 7  
 AAO30111  
 ID AAO30111 standard; peptide; 12 AA.  
 XX AC AAO30111;  
 XX DT 03-SEP-2003 (first entry)  
 XX DE Human beta globin biopolymer marker peptide.  
 XX KW Human; biopolymer marker; disease categorisation; insulin resistance;  
 KW acute Syndrome X; heart attack; stroke; therapy; beta globin.

XX OS Homo sapiens.  
 XX PN WO2003046556-A2.  
 XX PD 05-JUN-2003.  
 XX PF 31-OCT-2002; 2002WO-CA001657.  
 XX PR 23-NOV-2001; 2001US-00993343.  
 XX PA (SYNX-) SYN.X PHARMA INC.  
 XX PI Jackowski G, Marshall J;  
 XX DR WPI; 2003-523251/49.  
 XX PT Novel biopolymer marker or its analyte, useful for evidencing and  
 PT categorizing at least one disease state in a patient.  
 XX PS Claim 1; Page 43; 43pp; English.  
 XX CC The invention relates to a biopolymer marker or its analyte, useful for  
 CC evidencing and categorising at least one disease state in a patient. The  
 CC invention particularly relates to globin biopolymer markers indicative of  
 CC insulin resistance. Biopolymer marker is useful for evidencing and  
 CC categorising at least one disease state e.g. for predicting insulin  
 CC resistance. A diagnostic assay kit is useful for identifying therapeutic  
 CC avenues related to a disease state. Biopolymer markers are useful as  
 CC tools for rapidly and accurately diagnosing acute Syndrome X events such  
 CC as heart attack and stroke, and facilitate treatment. The present  
 CC sequence is human beta globin biopolymer marker peptide indicative of  
 CC insulin resistance  
 XX SQ Sequence 12 AA;  
 Query Match 100.0%; Score 58; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0018;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LVVYPWTQRF 10  
 Db 3 LVVYPWTQRF 12  
 RESULT 8  
 AAP50291  
 ID AAP50291 standard; protein; 74 AA.  
 XX AC AAP50291;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 30-NOV-1991 (first entry)  
 XX DE Sequence encoded by second exon of rabies glycoprotein gene.  
 XX KW Rabies vaccine; therapy; glycoprotein; antigen; diagnosis.  
 XX OS Rabies virus.  
 XX PN WO8501516-A.  
 XX PD 11-APR-1985.  
 XX PF 03-OCT-1983; 83FR-00015716.  
 XX PR 03-OCT-1983; 83FR-00015716.  
 XX PR 27-MAR-1984; 84FR-00004754.  
 XX PR 03-OCT-1984; 84FR-00015716.  
 XX PA (TRGE ) TRANSGENE SA.  
 PA (LATH/) LATHE R.  
 XX

PI	Lathe R, Kiény MP, Lemoine Y, Loison G, Aigle M;
XX	WPI; 1985-098845/16.
DR	N-PSDB; AAN50333.
XX	Vector for expressing rabies antigen - in eucaryotic cells, useful for
PT	making vaccines and curative agents.
XX	Example; Fig 10; 62pp; French.
PS	The inventors claim a vector for expressing a rabies antigen protein in
XX	eucaryotic cells. After glycosylation with a yeast (specifically at ASP
CC	residues 204 and 319), the recombinant antigen protein is useful as a
CC	vaccine or curative agent. The coding sequence in the vector can be
CC	followed by an intron (see AAN50333.N50334) or sites of polyadenylation.
CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	Sequence 74 AA;
QS	Query Match 100.0%; Score 58; DB 1; Length 74; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LVVYPWTORF 10 
DB	2 LVVYPWTORF 11 
RESULT 9	
AAR69602	AAR69602 standard; protein; 74 AA.
ID	AAR69602 standard; protein; 74 AA.
XX	AAR69602;
XX	25-MAR-2003 (revised)
DT	25-SEP-1995 (first entry)
XX	Human beta-globin encoded by optimised exon 2.
DE	Beta-globin; optimised codons; exon 2.
XX	Synthetic.
OS	WO9504744-A1.
PX	16-FEB-1995.
PD	29-JUL-1994; 94WO-US008630.
XX	11-AUG-1993; 93US-00105989.
XX	(DNXD-) DNX CORP.
PA	Kumar R, Sharma A, Paulhiac C, Khoury-Christianson AM, Midha S;
PI	WPI; 1995-090838/12.
XX	N-PSDB; AAQ83723.
DR	Production of human haemoglobin in transgenic pigs - by introducing gene
PT	constructs comprising human alpha and beta globin genes into pig ova, for
PT	an efficient source of haemoglobin for use in e.g. transfusions.
XX	Example; Fig 39; 155pp; English.
PS	Human alpha-globin is expressed in transgenic pigs at higher levels than
XX	human beta-globin. One approach to increasing the level of expressed beta
CC	-globin is to engineer the human beta-globin gene from the promoter
CC	region through the coding sequence and into the polyA site and 3' UTR to
CC	be similar to pig beta-globin gene, but without altering the AA sequence
CC	from that of authentic wt human beta-globin. PCR was used to optimise
CC	human beta-globin gene for porcine expression. Equivalent fragments of
CC	the human and pig beta-globin coding sequences in exons 1, 2 are 3 are
CC	depicted in AAQ83716/Q83719, AAQ83717/Q83720 and AAQ83718/Q83721,

CC	respectively. These pairs of sequences may be compared for differences.
CC	Optimised human beta-globin coding sequences for exons 1, 2 and 3 are
CC	depicted in AAQ83722, AAQ83723 and AAQ83724, respectively. These
CC	sequences may be compared with AAQ83716, AAQ83717 and AAQ83718
CC	respectively. The AA sequences encoded by the optimised human beta-globin
CC	coding sequences are given in AAR69601, AAR69602, AAR69603. (Updated on
CC	25-MAR-2003 to correct PN field.)
XX	Sequence 74 AA;
QS	Query Match 100.0%; Score 58; DB 2; Length 74; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LVVYPWTORF 10 
DB	2 LVVYPWTORF 11 
RESULT 10	
AAO07245	AAO07245 standard; protein; 86 AA.
ID	AAO07245 standard; protein; 86 AA.
XX	AAO07245;
AC	06-NOV-2001 (first entry)
DT	Human polypeptide SEQ ID NO 21137.
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation.
XX	Homo sapiens.
OS	WO200164835-A2.
PX	07-SEP-2001.
PD	26-FEB-2001; 2001WO-US004927.
XX	28-FEB-2000; 2000US-00515126.
PR	18-MAY-2000; 2000US-00577409.
XX	(HYSE-) HYSEQ INC.
XX	Tang YT, Liu C, Drmanac RT;
PI	WPI; 2001-514838/56.
XX	N-PSDB; AAI87176.
DR	Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT	and treating e.g. leukemia, inflammation and immune disorders.
XX	Claim 20; SEQ ID NO 21137; 1399pp + Sequence Listing; English.
PS	The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC	cytokines, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activity/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 86 AA;
QS	

Query Match 100.0%; Score 58; DB 4; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10  
 DB 39 LVVYPTQRF 48  
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RESULT 11  
 AAU30074  
 ID AAU30074 standard; protein; 104 AA.  
 AC AAU30074;  
 DT 18-DEC-2001 (first entry)  
 DE Novel human secreted protein #565.  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200179449-A2.  
 XX 25-OCT-2001.  
 PD 16-APR-2001; 2001WO-US008656.  
 PF 18-APR-2000; 2000US-00552929.  
 PR 26-JAN-2001; 2001US-00770160.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI; 2001-611725/70.  
 DR Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy.  
 XX Claim 20; Page 234; 765pp; English.  
 CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising the  
 CC nucleic acids encoding the polypeptides and cells genetically engineered  
 CC to express them are also useful for producing the proteins. The proteins  
 CC are useful in genetic vaccination, testing and therapy, and can be used  
 CC as nutritional supplements. They may be used to increase stem cell  
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
 CC and/or nerve tissue growth or regeneration; immune suppression and/or  
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human  
 CC secreted proteins of the invention  
 XX Sequence 104 AA;

Query Match 100.0%; Score 58; DB 4; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10  
 DB 33 LVVYPTQRF 42  
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RESULT 12  
 AAO02538  
 ID AAO02538 standard; protein; 110 AA.  
 AC AAO02538;  
 XX 06-NOV-2001 (first entry)  
 DE Human polypeptide SEQ ID NO 16430.  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200164835-A2.  
 XX 07-SEP-2001.  
 PD 26-FEB-2001; 2001WO-US004927.  
 PF 28-FEB-2000; 2000US-00515126.  
 PR 18-MAY-2000; 2000US-00577409.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI; 2001-514838/56.  
 DR N-PSDB; AAI82469.  
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX Claim 20; SEQ ID NO 16430; 1399pp + Sequence Listing; English.  
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 110 AA;  
 SQ Query Match 100.0%; Score 58; DB 4; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10  
 DB 17 LVVYPTQRF 26  
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RESULT 13  
 AAR89261  
 ID AAR89261 standard; peptide; 112 AA.  
 AC AAR89261;  
 XX 25-MAR-2003 (revised)  
 DT 04-MAR-1996 (first entry)  
 XX

```

DE XX Human beta-globin mutant Gln/Lys90 and Asp108.
KW XX Human beta-globin; mutant Gln/Lys90 and Asp108; hypoxic cells;
KW XX increased oxygenation; radiation therapy; vascular diseases.
XX XX
OS XX Homo sapiens.
FH XX Key Location/Qualifiers
FT XX Misc-difference 90
FT XX /label= Gln, Lys
XX XX
XX XX US5428007-A.
XX XX 27-JUN-1995.
XX XX
XX XX 28-APR-1994; 94US-00235118.
XX XX
XX XX 06-OCT-1989; 89US-00417949.
XX XX 09-OCT-1992; 92US-00959286.
XX XX
XX XX (UYVA ) UNIV YALE.
XX XX
XX XX Baserga SJ, Fischer JJ;
XX XX WPI; 1995-240064/31.
XX XX
XX XX Increasing tissue oxygen in hypoxic cells - by administering a pure
XX XX mutant alpha or beta haemoglobin having a low oxygen affinity.
XX XX
XX XX Example 3; Col 5-6; 10pp; English.
XX XX
XX XX AAR89262 is the human beta-globin mutant Val90, Met91, Ser93, Glu94. The
XX XX mutant globin can be used to increase tissue oxygenation in hypoxic
XX XX cells, to increase oxygenation in tumours to enhance the effects of
XX XX radiation therapy or as a blood replacement or treatment in vascular
XX XX diseases. (Updated on 25-MAR-2003 to correct PF field.)
XX XX
XX XX Sequence 112 AA;
XX XX
XX XX Query Match 100.0%; Score 58; DB 2; Length 112;
XX XX Best Local Similarity 100.0%; Pred. No. 0.02;
XX XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41
XX XX
RESULT 15
AAR89262
ID AAR89262 standard; peptide; 112 AA.
XX XX
XX XX AAG01752;
XX XX
XX XX 06-OCT-2000 (first entry)
XX XX
XX XX Human secreted protein, SEQ ID NO: 5833.
XX XX
XX XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX XX gene therapy; chromosome mapping.
XX XX
XX XX Homo sapiens.
XX XX
XX XX EP1033401-A2.
XX XX
XX XX 06-SEP-2000.
XX XX
XX XX 21-FEB-2000; 2000EP-00200610.
XX XX
XX XX 26-FEB-1999; 99US-0122487P.
XX XX
XX XX (GEST ) GENSET.
XX XX
XX XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX XX
XX XX WPI; 2000-500381/45.
XX XX
XX XX N-PSDB; AAC01758.
XX XX
XX XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX XX
XX XX Claim 13; SEQ ID NO 5833; 71pp + Sequence Listing; English.
XX XX
XX XX The present sequence is a polypeptide encoded by one of a large number of
XX XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can

```

CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

XX  
SQ Sequence 121 AA;

Query Match 100.0%; Score 58; DB 3; Length 121;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYEWTFQRF 10  
| | | | | | | |  
Db 33 LVVYEWTFQRF 42

Search completed: July 26, 2005, 10:59:46  
Job time : 166 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 10:51:13 ; Search time 43 Seconds  
(without alignments)  
17.360 Million cell updates/sec

Title: US-09-147-490-1  
Perfect score: 58  
Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/prodata/1/iaa/PCFUS\_COMB.pep.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	2	US-08-627-173-4
2	58	100.0	10	2	US-08-627-173-26
3	58	100.0	10	2	US-08-535-882A-4
4	58	100.0	10	2	US-08-535-882A-26
5	58	100.0	10	3	US-09-005-546-4
6	58	100.0	10	3	US-09-005-546-26
7	58	100.0	10	4	US-10-128-581-4
8	58	100.0	10	4	US-08-832-443C-4
9	58	100.0	38	4	US-08-453-485B-96
10	58	100.0	55	3	US-09-352-078-9
11	58	100.0	74	2	US-08-105-989-21
12	58	100.0	74	2	US-08-105-989-25
13	58	100.0	74	3	US-09-138-922-21
14	58	100.0	74	3	US-09-138-922-25
15	58	100.0	121	4	US-09-513-999C-5833
16	58	100.0	143	3	US-09-230-603-22
17	58	100.0	143	3	US-09-230-603-21
18	58	100.0	146	1	US-07-923-692C-10
19	58	100.0	146	1	US-08-170-095B-2
20	58	100.0	146	1	US-08-184-237-10
21	58	100.0	146	1	US-08-240-712-19
22	58	100.0	146	1	US-08-240-712-20
23	58	100.0	146	1	US-08-240-712-21
24	58	100.0	146	1	US-08-240-712-22
25	58	100.0	146	1	US-08-240-712-23
26	58	100.0	146	1	US-08-240-712-24
27	58	100.0	146	1	US-08-240-712-28

28	58	100.0	146	1	US-08-396-866-2	Sequence 2, Appli
29	58	100.0	146	1	US-08-443-890-19	Sequence 19, Appl
30	58	100.0	146	1	US-08-443-890-20	Sequence 20, Appl
31	58	100.0	146	1	US-08-443-890-21	Sequence 21, Appl
32	58	100.0	146	1	US-08-443-890-22	Sequence 22, Appl
33	58	100.0	146	1	US-08-443-890-23	Sequence 23, Appl
34	58	100.0	146	1	US-08-443-890-24	Sequence 24, Appl
35	58	100.0	146	1	US-08-443-890-28	Sequence 28, Appl
36	58	100.0	146	2	US-08-484-686B-66	Sequence 66, Appl
37	58	100.0	146	2	US-08-484-686B-67	Sequence 67, Appl
38	58	100.0	146	2	US-08-484-686B-68	Sequence 68, Appl
39	58	100.0	146	2	US-08-484-686B-70	Sequence 70, Appl
40	58	100.0	146	2	US-08-432-071B-4	Sequence 4, Appli
41	58	100.0	146	2	US-08-627-173-18	Sequence 18, Appl
42	58	100.0	146	2	US-08-627-173-22	Sequence 22, Appl
43	58	100.0	146	2	US-08-482-920-10	Sequence 10, Appl
44	58	100.0	146	2	US-08-535-882A-18	Sequence 18, Appl
45	58	100.0	146	2	US-08-535-882A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-08-627-173-4  
; Sequence 4, Application US/08627173  
; Patent No. 5861483  
; GENERAL INFORMATION:  
; APPLICANT: TSVILOVA, IRENA  
; APPLICANT: WOLPE, STEPHEN D.  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; TITLE OF INVENTION: USSES THEREOF  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,173  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/535,882  
; FILING DATE: 28-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1331-177  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-627-173-4

Query Match 100.0%; Score 58; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LVVYPWTQRF 10

Db 1 LVVYPWTQRF 10  
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RESULT 2  
US-08-627-173-26  
; Sequence 26, Application US/08627173  
; Patent No. 5861483  
; GENERAL INFORMATION:  
; APPLICANT: TSYRLOVA, IRENA  
; APPLICANT: WOLPE, STEPHEN D.  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,173  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/535,882  
; FILING DATE: 28-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1331-177  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4100  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 26:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-627-173-26  
Query Match 100.0%; Score 58; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LVVYPWTQRF 10  
Db 1 LVVYPWTQRF 10  
|||||  
RESULT 3  
US-08-535-882A-4  
; Sequence 4, Application US/08535882A  
; Patent No. 5939391  
; GENERAL INFORMATION:  
; APPLICANT: TSYRLOVA, IRENA  
; APPLICANT: WOLPE, STEPHEN D.  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA

; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,882A  
; FILING DATE: 28-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1331-177  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-535-882A-4  
Query Match 100.0%; Score 58; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LVVYPWTQRF 10  
Db 1 LVVYPWTQRF 10  
|||||  
RESULT 4  
US-08-535-882A-26  
; Sequence 26, Application US/08535882A  
; Patent No. 5939391  
; GENERAL INFORMATION:  
; APPLICANT: TSYRLOVA, IRENA  
; APPLICANT: WOLPE, STEPHEN D.  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,882A  
; FILING DATE: 28-SEP-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 1331-177  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-535-882A-26

Query Match 100.0%; Score 58; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 1 LVVYPTQRF 10

RESULT 5
US-09-005-546-4
; Sequence 4, Application US/09005546
; Patent No. 6090782
; GENERAL INFORMATION:
; APPLICANT: TSIRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: US$ THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US/09/005,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-005-546-4

Query Match 100.0%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 1 LVVYPTQRF 10

RESULT 6
US-09-005-546-26
; Sequence 26, Application US/09005546
; Patent No. 6090782
; GENERAL INFORMATION:
; APPLICANT: TSIRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: US$ THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-005-546-26

Query Match 100.0%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10
Db 1 LVVYPTQRF 10

RESULT 7
US-10-128-581-4
; Sequence 4, Application US/10128581
; Patent No. 6610654
; GENERAL INFORMATION:
; APPLICANT: TSIRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL
; FOR INHIBITING STEM CELL PROLIFERATION
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,581
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; FILING DATE: 24-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/617,840  
; FILING DATE: 17-JUL-2000  
; APPLICATION NUMBER: US 09/005,546  
; FILING DATE: 12-JAN-1998  
; APPLICATION NUMBER: US 08/535,882  
; FILING DATE: 28-SEP-1995  
; APPLICATION NUMBER: US 08/316,424  
; FILING DATE: 30-SEP-1994  
; APPLICATION NUMBER: PCT/US94/03349  
; FILING DATE: 29-MAR-1994  
; APPLICATION NUMBER: US 08/040,942  
; FILING DATE: 31-MAR-1993  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-128-581-4  
Query Match 100.0%; Score 58; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
Qy 1 LVVYPWTQRF 10  
Db 1 LVVYPWTQRF 10

RESULT 8  
US-08-832-443C-4  
; Sequence 4, Application US/08832443C  
; Patent No. 6784155  
; GENERAL INFORMATION:  
; APPLICANT: TSIRLOVA, IRENA  
; WOLPE, STEPHEN D.  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; USES THEREOF  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/832,443C  
; FILING DATE: 03-Apr-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/627,173  
; FILING DATE: 03-APR-1996  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-832-443C-4

Query Match 100.0%; Score 58; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00066; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
Qy 1 LVVYPWTQRF 10  
Db 1 LVVYPWTQRF 10

RESULT 9  
US-08-453-485E-96  
; Sequence 96, Application US/08453485E  
; Patent No. 6828125  
; GENERAL INFORMATION:  
; APPLICANT: Baxter Biotech Technology Sarl  
; TITLE OF INVENTION: DNA ENCODING FUSED DI-ALPHA GLOBINS AND USE THEREOF  
; FILE REFERENCE: BXTB 1885  
; CURRENT APPLICATION NUMBER: US/08/453,485E  
; CURRENT FILING DATE: 1995-05-30  
; PRIOR APPLICATION NUMBER: 07/789,179  
; PRIOR FILING DATE: 1991-11-08  
; PRIOR APPLICATION NUMBER: 07/671,707  
; PRIOR FILING DATE: 1991-04-01  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hemoglobin  
; OTHER INFORMATION: Cheverly (beta phe-> ser)  
US-08-453-485E-96  
Query Match 100.0%; Score 58; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0026; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
Qy 1 LVVYPWTQRF 10  
Db 23 LVVYPWTQRF 32

RESULT 10  
US-09-352-078-9  
; Sequence 9, Application US/09352078  
; Patent No. 6337314  
; GENERAL INFORMATION:  
; APPLICANT: Theragem, Inc.  
; APPLICANT: Hoffman, Brian F.  
; APPLICANT: Dubnick, Bernard  
; TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR  
; THE TREATMENT OF MICROBIAL INFECTIONS  
; FILE REFERENCE: 1944/1D999U1  
; CURRENT APPLICATION NUMBER: US/09/352,078  
; CURRENT FILING DATE: 1999-07-14  
; EARLIER APPLICATION NUMBER: PCT/US98/16746  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/061,454  
; EARLIER FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-352-078-9  
Query Match 100.0%; Score 58; DB 3; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0037; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
Qy 1 LVVYPWTQRF 10

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Db          32 LVVYPWTQRF 41
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RESULT 11
US-08-105-989-21
; Sequence 21, Application US/08105989
; Patent No. 5922854
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; TITLE OF INVENTION: Production of Human Hemoglobin in
; TITLE OF INVENTION: Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6794-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-105-989-21

Query Match      100.0%; Score 58; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LVVYPWTQRF 10
Db          2 LVVYPWTQRF 11
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RESULT 13
US-09-138-922-21
; Sequence 21, Application US/09138922
; Patent No. 6147202
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; TITLE OF INVENTION: Production of Human Hemoglobin in
; TITLE OF INVENTION: Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,922
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/105,989
; FILING DATE: 11-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.

Qy          1 LVVYPWTQRF 10
Db          2 LVVYPWTQRF 11
|||||
RESULT 12
US-08-105-989-25
; Sequence 25, Application US/08105989
; Patent No. 5922854
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Sharma, Ajay
; APPLICANT: Paulhiac, Clara
; APPLICANT: Khoury-Christianson, Anastasia P.
; TITLE OF INVENTION: Production of Human Hemoglobin in
; TITLE OF INVENTION: Transgenic Pigs.
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
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; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6794-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 74 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-138-922-21

Query Match 100.0%; Score 58; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 0.005;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
Db 2 LVVYPWTQRF 11

RESULT 14  
US-09-138-922-25  
; Sequence 25, Application US/09138922  
; Patent No. 6147202  
; GENERAL INFORMATION:

; APPLICANT: Kumar, Ramesh  
; APPLICANT: Sharma, Ajay  
; APPLICANT: Paulhiac, Clara  
; APPLICANT: Khoury-Christianson, Anastasia P.  
; APPLICANT: Midha, Sunita

; TITLE OF INVENTION: Production of Human Hemoglobin in  
; TRANSGENIC PIGS.

; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/138,922  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,989  
; FILING DATE: 11-AUG-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 6794-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 74 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-138-922-25

Query Match 100.0%; Score 58; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 0.005;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LVVYPWTQRF 10  
Db 2 LVVYPWTQRF 11

# RESULT 15

US-09-513-999C-5833  
; Sequence 5833, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 5833

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-513-999C-5833

Query Match 100.0%; Score 58; DB 4; Length 121;  
Best Local Similarity 100.0%; Pred. No. 0.0083;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
Db 33 LVVYPWTQRF 42

Search completed: July 26, 2005, 11:01:18  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 10:53:58 ; Search time 156 Seconds  
(without alignments)  
24.935 Million cell updates/sec

Title: US-09-147-490-1  
Perfect score: 58  
Sequence: 1 LVVPTQRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues  
Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	58	100.0	10	14	US-10-128-581-4
3	58	100.0	10	15	US-10-463-699-4
4	58	100.0	10	16	US-10-776-172-4
5	58	100.0	10	17	US-10-485-518A-3
6	58	100.0	10	17	US-10-897-005-4
7	58	100.0	140	15	US-10-363-616-477
8	58	100.0	146	9	US-09-839-164-4
9	58	100.0	146	9	US-09-839-164-8
10	58	100.0	146	9	US-09-977-577-15
11	58	100.0	146	9	US-09-977-577-16

12	58	100.0	146	9	US-09-977-577-17	Sequence 17, Appl
13	58	100.0	146	9	US-09-977-577-20	Sequence 20, Appl
14	58	100.0	146	13	US-10-085-853-33	Sequence 33, Appl
15	58	100.0	146	14	US-10-128-581-23	Sequence 23, Appl
16	58	100.0	146	14	US-10-128-581-27	Sequence 27, Appl
17	58	100.0	146	15	US-10-463-699-25	Sequence 25, Appl
18	58	100.0	146	15	US-10-463-699-29	Sequence 29, Appl
19	58	100.0	146	15	US-10-463-699-25	Sequence 3019, Ap
20	58	100.0	146	16	US-10-776-172-18	Sequence 18, Appl
21	58	100.0	146	16	US-10-776-172-22	Sequence 22, Appl
22	58	100.0	146	17	US-10-897-005-25	Sequence 25, Appl
23	58	100.0	146	17	US-10-897-005-29	Sequence 29, Appl
24	58	100.0	146	17	US-10-897-005-29	Sequence 15, Appl
25	58	100.0	146	17	US-10-897-005-25	Sequence 16, Appl
26	58	100.0	146	17	US-10-897-005-25	Sequence 17, Appl
27	58	100.0	146	17	US-10-897-005-25	Sequence 20, Appl
28	58	100.0	147	9	US-09-977-577-21	Sequence 21, Appl
29	58	100.0	147	16	US-10-723-860-125	Sequence 125, App
30	58	100.0	147	17	US-10-897-005-25	Sequence 21, Appl
31	58	100.0	148	14	US-10-280-679B-10	Sequence 10, Appl
32	58	100.0	148	15	US-10-280-679B-10	Sequence 10, Appl
33	55	94.8	146	9	US-09-839-164-6	Sequence 6, Appl
34	55	94.8	146	14	US-10-128-581-25	Sequence 25, Appl
35	55	94.8	146	15	US-10-463-699-27	Sequence 27, Appl
36	55	94.8	146	16	US-10-408-765A-84	Sequence 84, Appl
37	55	94.8	146	16	US-10-776-172-20	Sequence 20, Appl
38	55	94.8	146	17	US-10-897-005-27	Sequence 27, Appl
39	55	94.8	147	9	US-09-147-490-8	Sequence 8, Appl
40	54	93.1	9	15	US-10-237-405-2	Sequence 2, Appl
41	54	93.1	147	17	US-10-874-706-43	Sequence 43, Appl
42	52	89.7	9	14	US-10-128-581-5	Sequence 5, Appl
43	52	89.7	9	15	US-10-463-699-5	Sequence 5, Appl
44	52	89.7	9	16	US-10-776-172-5	Sequence 5, Appl
45	52	89.7	9	17	US-10-897-005-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-147-490-1  
; Sequence 1, Application US/09147490  
; Patent No. US20020147129A1  
; GENERAL INFORMATION:  
; APPLICANT: MENDELSON, FREDERICK A.O.  
; APPLICANT: CHAI, SIEM YEEN  
; APPLICANT: MOELLER, INGRID  
; APPLICANT: ALDRED, PETER G.  
; APPLICANT: SMITH, IAN A.  
; TITLE OF INVENTION: NEUROACTIVE PEPTIDE  
; FILE REFERENCE: 016786/0215  
; CURRENT APPLICATION NUMBER: US/09/147,490  
; CURRENT FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: PCT/AU97/00436  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: AU P00893  
; PRIOR FILING DATE: 1996-07-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 10  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Beta globin  
; OTHER INFORMATION: precursor  
US-09-147-490-1

Query Match 100.0%; Score 58; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0056;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10  
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 Db 1 LVVYPTQRF 10

## RESULT 2

US-10-128-581-4  
 ; Sequence 4, Application US/10128581  
 ; Publication No. US20030104984A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSYRLOVA, IRENA  
 ; WOLPE, STEPHEN D.  
 ; TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL  
 ; FOR INHIBITING STEM CELL PROLIFERATION

NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,581  
 FILING DATE: 24-APR-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/617,840  
 FILING DATE: 17-JUL-2000  
 APPLICATION NUMBER: US 09/005,546  
 FILING DATE: 12-JAN-1998  
 APPLICATION NUMBER: US 08/535,882  
 FILING DATE: 28-SEP-1995  
 APPLICATION NUMBER: US 08/316,424  
 FILING DATE: 30-SEP-1994  
 APPLICATION NUMBER: PCT/US94/03349  
 FILING DATE: 29-MAR-1994  
 APPLICATION NUMBER: US 08/040,942  
 FILING DATE: 31-MAR-1993

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid

STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 100.0%; Score 58; DB 14; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0056;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10  
 |||||  
 Db 1 LVVYPTQRF 10

## RESULT 3

US-10-463-699-4  
 ; Sequence 4, Application US/10463699  
 ; Publication No. US20040081640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSYRLOVA, IRENA  
 ; WOLPE, STEPHEN D.  
 ; TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS  
 ; USEFUL FOR INHIBITING STEM CELL PROLIFERATION  
 ; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 1.44 MB Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/463,699  
 FILING DATE: 18-Jun-2003  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 10/128,581  
 FILING DATE: 24-APR-2002  
 APPLICATION NUMBER: US 09/617,840  
 FILING DATE: 17-JUL-2000  
 APPLICATION NUMBER: US 09/005,546  
 FILING DATE: 12-JAN-1998  
 APPLICATION NUMBER: US 08/535,882  
 FILING DATE: 28-SEP-1995  
 APPLICATION NUMBER: US 08/316,424  
 FILING DATE: 30-SEP-1994  
 APPLICATION NUMBER: PCT/US94/03349  
 FILING DATE: 29-MAR-1994  
 APPLICATION NUMBER: US 08/040,942  
 FILING DATE: 31-MAR-1993

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid

STRANDEDNESS: <Unknown>  
 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 100.0%; Score 58; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0056;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPTQRF 10  
 |||||  
 Db 1 LVVYPTQRF 10

## RESULT 4

US-10-776-172-4  
 ; Sequence 4, Application US/10776172  
 ; Publication No. US20040167060A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSYRLOVA, IRENA  
 ; WOLPE, STEPHEN D.  
 ; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
 ; USES THEREOF

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: U.S.A.  
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MS Word

CURRENT APPLICATION DATA:



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; APPLICATION NUMBER: US/10/776,172
; FILING DATE: 12-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/627,173
; FILING DATE: 03-APR-1996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-776-172-4
Query Match 100.0%; Score 58; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10

RESULT 5
US-10-485-518A-3
; Sequence 3, Application US/10485518A
; GENERAL INFORMATION:
; APPLICANT: Howard Florey Institute of Experimental Physiology and Medicine
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE ACTIVITY
; FILE REFERENCE: P42903
; CURRENT APPLICATION NUMBER: US/10/485,518A
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: PCT/AU02/01034
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: Australian PR6722
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-485-518A-3
Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10

RESULT 6
US-10-897-005-4
; Sequence 4, Application US/10897005
; Publication No. US20050043218A1
; GENERAL INFORMATION:
; APPLICANT: TSVRLOVA, IRENA
; TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS
USEFUL FOR INHIBITING STEM CELL PROLIFERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSER: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

; APPLICATION NUMBER: US/10/776,172
; FILING DATE: 12-Feb-2004
; CLASSIFICATION: <Unknown>
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/897,005
; FILING DATE: 23-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 10/128,581
; FILING DATE: 24-APR-2002
; APPLICATION NUMBER: US 09/617,840
; FILING DATE: 17-JUL-2000
; APPLICATION NUMBER: US 09/005,546
; FILING DATE: 12-JAN-1998
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; APPLICATION NUMBER: US 08/316,424
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: PCT/US94/03349
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 08/040,942
; FILING DATE: 31-MAR-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-897-005-4
Query Match 100.0%; Score 58; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 1 LVVYPWTQRF 10

RESULT 7
US-10-363-616-477
; Sequence 477, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 477
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-477
Query Match 100.0%; Score 58; DB 15; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 8
US-09-839-164-4
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; Sequence 4, Application US/09839164
; Patent No. US20020098583A1
; GENERAL INFORMATION:
; APPLICANT: KOZLOV, VLADIMIR
; TSIRLOVA, IRENA
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,164
; FILING DATE: 23-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,668
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/316,424
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: PCT/US94/03349
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 08/040,942
; FILING DATE: 31-MAR-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-164-4

Query Match 100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 9
US-09-839-164-8
; Sequence 8, Application US/09839164
; Patent No. US20020098583A1
; GENERAL INFORMATION:
; APPLICANT: KOZLOV, VLADIMIR
; TSIRLOVA, IRENA
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8th FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,164
; FILING DATE: 23-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,668
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/316,424
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: PCT/US94/03349
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 08/040,942
; FILING DATE: 31-MAR-1993
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-839-164-8

Query Match 100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 10
US-09-977-577-15
; Sequence 15, Application US/09977577
; Patent No. US2002015595A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: MOLLER, Holger J.
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES TH
; FILE REFERENCE: MOESTRUP=1A
; CURRENT APPLICATION NUMBER: US/09/977,577
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: US 60/270,120
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: DK PA 2001 00039
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: DK PA 2000 01543
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-577-15

Query Match 100.0%; Score 58; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 11
US-09-977-577-16
; Sequence 16, Application US/09977577
; Patent No. US2002015595A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
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Wed Jul 27 09:27:25 2005

; APPLICANT: MOLLER, Holger J.  
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES THEREOF  
; FILE REFERENCE: MOESTRUP=1A  
; CURRENT APPLICATION NUMBER: US/09/977,577  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: US 60/270,120  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: DK PA 2001 00039  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: DK PA 2000 01543  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 16  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-977-577-16

Query Match 100.0%; Score 58; DB 9; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.067; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
Db 32 LVVYPWTQRF 41

RESULT 12  
US-09-977-577-17  
; Sequence 17, Application US/09977577  
; Patent No. US20020155995A1  
; GENERAL INFORMATION:  
; APPLICANT: MOESTRUP, Soren  
; APPLICANT: MOLLER, Holger J.  
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES THEREOF  
; FILE REFERENCE: MOESTRUP=1A  
; CURRENT APPLICATION NUMBER: US/09/977,577  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: US 60/270,120  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: DK PA 2001 00039  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: DK PA 2000 01543  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 17  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-977-577-17

Query Match 100.0%; Score 58; DB 9; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.067; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
Db 32 LVVYPWTQRF 41

RESULT 13  
US-09-977-577-20  
; Sequence 20, Application US/09977577  
; Patent No. US20020155995A1  
; GENERAL INFORMATION:  
; APPLICANT: MOESTRUP, Soren  
; APPLICANT: MOLLER, Holger J.  
; TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES THEREOF  
; FILE REFERENCE: MOESTRUP=1A  
; CURRENT APPLICATION NUMBER: US/09/977,577  
; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: US 60/270,120  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: DK PA 2001 00039  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: DK PA 2000 01543  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 20  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-977-577-20

Query Match 100.0%; Score 58; DB 9; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.067; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
Db 32 LVVYPWTQRF 41

RESULT 14  
US-10-085-853-33  
; Sequence 33, Application US/10085853  
; Publication No. US20020194643A1  
; GENERAL INFORMATION:  
; APPLICANT: Merot, Bertrand  
; APPLICANT: Dieryck, Wilfrid  
; APPLICANT: Lence, Philippe  
; APPLICANT: Marden, Michael  
; APPLICANT: Gruber, Veronique  
; APPLICANT: Pagnier, Renee-Josée  
; APPLICANT: Baudino, Sylvie  
; APPLICANT: Poyart, Claude  
; TITLE OF INVENTION: METHOD FOR PRODUCING HAEMIN PROTEINS USING PLANT  
; TITLE OF INVENTION: CELLS,  
; TITLE OF INVENTION: RESULTING PROTEINS AND PRODUCTS CONTAINING SAME  
; FILE REFERENCE: 8076.147USWO  
; CURRENT APPLICATION NUMBER: US/10/085,853  
; CURRENT FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: 08/983,564  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: PCT/FR96/01123  
; PRIOR FILING DATE: 1996-07-17  
; PRIOR APPLICATION NUMBER: 95/08615  
; PRIOR FILING DATE: 1995-07-17  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-085-853-33

Query Match 100.0%; Score 58; DB 13; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.067; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
Db 32 LVVYPWTQRF 41

RESULT 15  
US-10-128-581-23  
; Sequence 23, Application US/10128581  
; Publication No. US20030104984A1  
; GENERAL INFORMATION:  
; APPLICANT: TSYRLOVA, IRENA  
; APPLICANT: WOLPE, STEPHEN D.  
; TITLE OF INVENTION: HEMOGLOBIN ALPHA CHAIN PEPTIDE FRAGMENTS USEFUL

## FOR INHIBITING STEM CELL PROLIFERATION

NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,581  
FILING DATE: 24-Apr-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/617,840  
FILING DATE: 17-JUL-2000  
APPLICATION NUMBER: US 09/005,546  
FILING DATE: 12-JAN-1998  
APPLICATION NUMBER: US 08/535,882  
FILING DATE: 28-SEP-1995  
APPLICATION NUMBER: US 08/316,424  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: PCT/US94/03349  
FILING DATE: 29-MAR-1994  
APPLICATION NUMBER: US 08/040,942  
FILING DATE: 31-MAR-1993

## INFORMATION FOR SEQ ID NO: 23:

## SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-10-128-581-23

Query Match 100.0%; Score 58; DB 14; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
Db 32 LVVYPWTQRF 41

Search completed: July 26, 2005, 11:04:00  
Job time : 157 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 26, 2005, 10:50:07 ; Search time 39 Seconds  
(without alignments)  
24.671 Million cell updates/sec

Title: US-09-147-490-1  
Perfect score: 58  
Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	61	4 I65317	hemoglobin delta c
2	58	100.0	61	4 I52502	hemoglobin beta c
3	58	100.0	110	4 I46172	hypothetical hemog
4	58	100.0	122	2 A05304	hemoglobin beta-1
5	58	100.0	141	1 HBMF	hemoglobin beta-C
6	58	100.0	141	1 HBHCR	hemoglobin beta-C
7	58	100.0	141	1 HBGTC	hemoglobin beta-C
8	58	100.0	142	1 HBHSC	hemoglobin beta c
9	58	100.0	145	1 HBBOB	hemoglobin beta-A
10	58	100.0	145	1 HBBOB	hemoglobin beta-A
11	58	100.0	145	1 HBBOF	hemoglobin beta c
12	58	100.0	145	1 HBBOG	hemoglobin beta c
13	58	100.0	145	1 HBBOA	hemoglobin beta c
14	58	100.0	145	1 HBDE3	hemoglobin beta-II
15	58	100.0	145	1 HBEXN	hemoglobin beta c
16	58	100.0	145	1 HBGTA	hemoglobin beta-A
17	58	100.0	145	1 HBGTF	hemoglobin beta c
18	58	100.0	145	1 HBHSA	hemoglobin beta-A
19	58	100.0	145	1 HBHSH	hemoglobin beta-B
20	58	100.0	145	1 HBVA2	hemoglobin beta c
21	58	100.0	145	1 HGSH	hemoglobin beta c
22	58	100.0	145	2 S13609	hemoglobin beta c
23	58	100.0	145	2 C25727	hemoglobin beta c
24	58	100.0	145	2 B58794	hemoglobin beta c
25	58	100.0	146	1 HDGI	hemoglobin delta c
26	58	100.0	146	1 B61434	hemoglobin beta c
27	58	100.0	146	1 HBHAG	hemoglobin beta c
28	58	100.0	146	1 HBHAM	hemoglobin beta c
29	58	100.0	146	1 HBBAV	hemoglobin beta c

ALIGNMENTS

RESULT 1

I65317  
hemoglobin delta chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 12-Jul-1996 #sequence\_revision 31-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: I65317  
R:Li, J.-Z.; Harano, T.; Lancelos, K.D.; Huismann, T.H.  
Biochim. Biophys. Acta 909, 208-212, 1987  
A:Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-  
A:Reference number: I52502; MUID:87299720; PMID:3620470  
A:Accession: I65317  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-61 <LU>  
A:Cross-references: UNIPROT:Q14485; GB:M25661; NID:G183863; PIDN:AAA53154.1; PID:G183864  
A:Note: this sequence was not determined in this report  
C:Genetics:  
A:Gene: GDB:HBD  
A:Cross-references: GDB:119298  
A:Map position: 11p15.5-11p15.5  
A:Introns: 31/3

Query Match 100.0%; Score 58; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
|||  
DB 33 LVVYPWTQRF 42

RESULT 2

I52502  
hemoglobin beta chain - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 02-Jul-1996 #sequence\_revision 31-Jul-1997 #text\_change 09-Jul-2004  
C:Accession: I52502  
R:Li, J.-Z.; Harano, T.; Lancelos, K.D.; Huismann, T.H.  
Biochim. Biophys. Acta 909, 208-212, 1987  
A:Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-  
A:Reference number: I52502; MUID:87299720; PMID:3620470  
A:Accession: I52502  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-61 <LU>  
A:Cross-references: UNIPROT:Q14484; GB:M25660; NID:G183856; PIDN:AAA53153.1; PID:G183857  
A:Note: this sequence was not determined in this report  
C:Genetics:  
A:Gene: GDB:HBB  
A:Cross-references: GDB:119297  
A:Map position: 11p15.4-11p15.4  
A:Introns: 31/3

```
Query Match      100.0%; Score 58; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 3
I46172
hypothetical hemoglobin psi-beta-z pseudogene - goat (fragment)
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
C:Accession: I46172
R:Clearay, M.L.; Schon, E.A.; Lingrel, J.B.
Cell 26, 181-190, 1981
A:Title: Two related pseudogenes are the result of a gene duplication in the goat beta-globin cluster
A:Reference number: I46172; MUID:82137052; PMID:7332927
A:Accession: I46172
A>Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene
A:Molecule type: DNA
A:Residues: 1-110 <CLE>
A:Cross-references: EMBL:V00154; NID:g965; PIDN:CAA23469.1; PID:g966
C:Genetics:
A:Introns: 11/3; 18/3; 29/2; 103/3
C:Keywords: pseudogene

Query Match      100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 31 LVVYPWTQRF 40

RESULT 4
A05304
hemoglobin beta-1 chain - Indian spiny-tailed lizard (tentative sequence) (fragments)
C:Species: Uromastix hardwickii (Indian spiny-tailed lizard)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 12-Jul-2004
C:Accession: A05304
R:Nagvi, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jornvall, H.
FEBS Lett. 162, 290-295, 1983
A:Reference number: A91314; MUID:84029159; PMID:6628672
A:Accession: A05304
A:Molecule type: protein
A:Residues: 1-122 <NAO>
A:Cross-references: UNIPROT:P18991
A>Note: the peptides were positioned by homology
C:Superfamily: Globin; Globin homology
C:Keywords: chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-122/Domain: globin homology (fragments) <GLB>
F:80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match      100.0%; Score 58; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 5
HBMFC
hemoglobin beta-C chain - mouflon (tentative sequence)
C:Species: Ovis orientalis musimon, Ovis ammon musimon (mouflon)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Jul-2004
C:Accession: A90232; A02396
R:Wilson, J.B.; Miller, A.; Huismann, T.H.J.
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Biochem. Genet. 4, 677-688, 1970
A:Title: Production of hemoglobin C in the mouflon (Ovis musimon pallas, 1811) and the l
pides from the beta(B) and beta (C) chains"
A:Reference number: A90232; MUID:71089262; PMID:5496230
A:Accession: A90232
A:Molecule type: protein
A:Residues: 1-141 <WIL>
A>Note: compositions of tryptic peptides were determined; positions 100-111 were sequence
C:Comment: This type of beta-C chain is found when anemia has been experimentally produce
C:Superfamily: globin; Globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match      100.0%; Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 27 LVVYPWTQRF 36

RESULT 6
HBSHCR
hemoglobin beta-C chain - aoudad (tentative sequence)
C:Species: Ammotragus lervia (aoudad, Barbary Sheep)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Jul-2004
C:Accession: B90232; A02396
R:Wilson, J.B.; Miller, A.; Huismann, T.H.J.
Biochem. Genet. 4, 677-688, 1970
A:Title: Production of hemoglobin C in the mouflon (Ovis musimon pallas, 1811) and the l
pides from the beta(B) and beta (C) chains.
A:Reference number: A90232; MUID:71089262; PMID:5496230
A:Accession: B90232
A:Molecule type: protein
A:Residues: 1-141 <WIL>
A>Note: compositions of tryptic peptides were determined; positions 100-111 were sequence
C:Comment: This type of beta-C chain is found when anemia has been experimentally produce
C:Superfamily: globin; Globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match      100.0%; Score 58; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 27 LVVYPWTQRF 36

RESULT 7
HBGTC
hemoglobin beta-C chain - goat
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 12-Jul-2004
C:Accession: B02396; I46277; A02396
R:Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.
Cell 27, 359-369, 1981
A:Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: three
A:Reference number: A90817; MUID:82137075; PMID:6277503
A:Accession: B02396
A:Molecule type: DNA
A:Residues: 1-141 <SCH>
A:Cross-references: UNIPROT:P02078; GB:M15389
A>Note: initiator Met not shown
R:Haynes, J.R.; Rosteck, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; Ling
J. Biol. Chem. 255, 6355-6367, 1980
A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumptive
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A;Reference number: 146273; MUID:80227766; PMID:6248519  
 A;Accession: 146277  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 66-93, 'XX', 96-115, 'XX', 118-134 <HAY>  
 A;Cross-references: GB:K00662; NID:g164154; PID:g164158  
 C;Comment: This type of beta-C chain is found when anemia has been experimentally produced  
 C;Genetics:  
 A;Introns: 26/2; 100/3  
 C;Superfamily: globin; globin homology  
 C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
 F;1-141/Domain: globin homology <GLB>  
 F;58/Binding site: oxygen (His) (distal axial ligand) #status predicted  
 F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 0.0066;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
 DB 27 LVVYPWTQRF 36  
 |||||

RESULT 8  
 HBShc  
 hemoglobin beta-C chain - sheep  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Jan-1998 #text\_change 12-Jul-2004  
 C;Accession: S10074; B92027; A90045; A02396  
 R;Garner, K.J.; Lingrel, J.B.  
 J. Mol. Evol. 28, 175-184, 1989  
 A;Title: A comparison of the beta(A)- and beta(B)-globin gene clusters of sheep.  
 A;Reference number: S10073; MUID:89178744; PMID:2494347  
 A;Accession: S10074  
 A;Molecule type: DNA  
 A;Residues: 1-142 <GAR>  
 A;Cross-references: UNIPROT:P02079; EMBL:X14728; NID:gl212; PIDN:CAA32850.1; PID:g1213  
 A;Note: The authors translated the codon GTC for residue 30 as Ala  
 A;Note: the sequence of codons and residues 41-60 is repeated twice in the authors' translation.  
 R;Boyer, S.H.; Hathaway, P.; Pascasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.  
 J. Biol. Chem. 242, 2211-2232, 1967  
 A;Title: Differences in the amino acid sequences of tryptic peptides from three sheep hemoglobins.  
 A;Reference number: A92027; MUID:67134347; PMID:6022868  
 A;Accession: B92027  
 A;Molecule type: protein  
 A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'Z'  
 A;Experimental source: Dorset breed  
 R;Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huismann, T.H.J.  
 Arch. Biochem. Biophys. 115, 385-400, 1966  
 A;Title: The structure of sheep hemoglobins. II. The amino acid composition of the tryptic peptides.  
 A;Reference number: A90045  
 A;Accession: A90045  
 A;Molecule type: protein  
 A;Residues: 2-64, 'B', 66-68, 'B', 70-71, 'Z', 73-74, 'BB', 77-82, 'Z', 84-85, 'Z', 87-94, 'B', 96, 'Z'  
 A;Experimental source: Rambouillet breed  
 A;Note: there are several discrepancies between the sequence in this paper and that given in the literature.  
 C;Comment: This beta-C chain is produced when anemia is experimentally induced.  
 C;Genetics:  
 A;Introns: 26/2; 100/3  
 C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to form hemoglobin.  
 C;Function:  
 C;Superfamily: globin; globin homology  
 C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein  
 F;1-142/Domain: globin homology <GLB>  
 F;2-142/Product: hemoglobin beta-C chain #status experimental <MAT>  
 F;59/Binding site: oxygen (His) (distal axial ligand) #status predicted  
 F;88/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 0.0066;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
 DB 28 LVVYPWTQRF 37  
 |||||

## RESULT 9

## HBBOB

hemoglobin beta chain [validated] - bovine  
 N;Alternate names: hemoglobin-derived opioid peptide  
 N;Contains: LVV-hemorphin-7; WV-hemorphin-7  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 24-Apr-1984 #sequence\_revision 25-Feb-1985 #text\_change 12-Jul-2004  
 C;Accession: B93504; A90046; B90046; A90052; S35696; S65609; A02387  
 R;Schimenti, J.C.; Duncan, C.H.  
 Nucleic Acids Res. 12, 1641-1655, 1984  
 A;Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeat  
 A;Reference number: A93504; MUID:84144058; PMID:6322113  
 A;Accession: B93504  
 A;Molecule type: DNA  
 A;Residues: 1-145 <SCI>  
 A;Cross-references: UNIPROT:P02070; EMBL:X00376; NID:g394; PIDN:CAA25111.1; PID:g395  
 A;Experimental source: beta A allele, Jersey cattle  
 R;Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Robberson, B.; Babin, D.R.  
 Arch. Biochem. Biophys. 120, 124-135, 1967  
 A;Title: A comparison of amino acid sequences in the beta-chains of adult bovine hemoglobin.  
 A;Reference number: A90046; MUID:68001834; PMID:6048711  
 A;Accession: A90046  
 A;Molecule type: protein  
 A;Residues: 1-145 <SCL>  
 A;Experimental source: beta A allele, Jersey cattle  
 A;Accession: B90046  
 A;Molecule type: protein  
 A;Residues: 1-14, 'S', 16-17, 'H', 19-118, 'N', 120-145 <SCR2>  
 A;Experimental source: beta B allele, Jersey cattle  
 R;Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Apell, G.; Huismann, T.H.J.; Smith, L.L.; Arch. Biochem. Biophys. 152, 222-236, 1972  
 A;Title: Amino acid sequences in the beta-chains of adult bovine hemoglobins C-Rhodesia  
 A;Reference number: A90052; MUID:73007895; PMID:4561255  
 A;Accession: A90052  
 A;Molecule type: protein  
 A;Residues: 1-130, 'Q', 132-145 <SCR3>  
 A;Experimental source: C-Rhodesia allele, Angoni cattle (East African short-horn zebu)  
 A;Accession: B90052  
 A;Molecule type: protein  
 A;Residues: 1-19, 'G', 21-42, 'T', 44-145 <SCR4>  
 A;Experimental source: D-Zambia allele, Angoni cattle (East African short-horn zebu)  
 R;Barthudaryan, N.; Kellermann, J.; Galoyan, A.; Lottspeich, F.  
 FEBS Lett. 329, 215-218, 1993  
 A;Title: High molecular weight aspartic endopeptidase generates a coronar-constrictory  
 A;Reference number: S35696; MUID:93359052; PMID:8354398  
 A;Accession: S35696  
 A;Molecule type: protein  
 A;Residues: 31-40 <BAR>  
 A;Note: LVV-hemorphin-7 acts as a vasoconstrictor  
 R;Aubes-Dufau, I.; Capevieille, J.; Seris, J.L.; Combes, D.  
 FEBS Lett. 364, 115-119, 1995  
 A;Title: Bitter peptide from hemoglobin hydrolysate: isolation and characterization.  
 A;Reference number: S65609; MUID:95269781; PMID:7750554  
 A;Accession: S65609  
 A;Molecule type: protein  
 A;Residues: 32-40 <AUB>  
 A;Note: WV-hemorphin-7 isolated from a hydrolysate has a bitter taste  
 R;Perni, G.  
 Submitted to the Brookhaven Protein Data Bank, May 1993  
 A;Reference number: A52353; PDB:1HDA  
 A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 1-145  
 R;Perni, M.F.; Perni, G.; Poyart, C.; Pagnier, J.; Kister, J.  
 J. Mol. Biol. 233, 536-545, 1993  
 A;Title: A novel allosteric mechanism in haemoglobin. Structure of bovine deoxyhaemoglobin  
 n haemoglobin.  
 A;Reference number: A58463; MUID:94016570; PMID:8411160  
 A;Contents: annotation; X-ray crystallography, 2.2 angstroms

C;Genetics:  
A;Introns: 28/2; 102/3  
C;Complex: Two beta chains combine to form heterotetramers with two alpha chains to form  
C;Function:  
A;Description: in erythrocytes binds and transports molecular oxygen from lung to tissue  
C;Superfamily: globin; globin homology  
C;Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein  
F;2-145/Domain: globin homology <GLB>  
F;31-40/Product: LVV-hemophrin-7 #status experimental <OPTA>  
F;32-40/Product: VV-hemophrin-7 #status experimental <OPT9>  
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
| | | | | | | |  
DB 31 LVVYPWTQRF 40

RESULT 10  
HBBOB  
hemoglobin beta-A chain - banteng (tentative sequence)  
C;Species: Bos javanicus (banteng)  
C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 12-Jul-2004  
C;Accession: A02388  
R;Nanikawa, T.; Takenaka, O.; Takahashi, K.  
Biochem. Genet. 21, 787-796, 1983  
A;Title: Hemoglobin Bali (bovine): beta(A)18(B1)Lys -> His: one of the "missing links" B  
A;Reference number: A02388; MUID:84023669; PMID:6626147  
A;Accession: A02388

A;Molecule type: protein  
A;Residues: 1-145 <NAM>  
A;Cross-references: UNIPROT:P04346  
A;Experimental source: Hereford breed  
A;Note: tryptic peptides were positioned by homology with the bovine sequence  
C;Superfamily: globin; globin homology  
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
F;2-145/Domain: globin homology <GLB>  
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
| | | | | | | |  
DB 31 LVVYPWTQRF 40

RESULT 11  
HBBOF  
hemoglobin beta chain, fetal - bovine  
N;Alternate names: hemoglobin gamma chain  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 12-Jul-2004  
C;Accession: A03504; A0549; A02398  
R;Schimenti, J.C.; Duncan, C.H.  
Nucleic Acids Res. 12, 1641-1655, 1984

A;Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeat  
A;Reference number: A03504; MUID:84144058; PMID:6322113  
A;Accession: A03504

A;Molecule type: DNA  
A;Residues: 1-145 <SCH>  
A;Cross-references: UNIPROT:P02081; GB:X00354; NID:g392; PIDN:CAA25101.1; PID:g393  
R;Babin, D.R.; Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Robberson, B.  
Biochemistry 5, 1297-1310, 1966

A;Title: The amino acid sequence of the gamma chain of bovine fetal hemoglobin.  
A;Reference number: A0549; MUID:67089183; PMID:5958205  
A;Accession: A0549

A;Molecule type: protein  
A;Residues: 1-145 <BAB>  
C;Genetics:  
A;Introns: 29/2; 103/3  
C;Superfamily: globin; globin homology  
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
F;2-145/Domain: globin homology <GLB>  
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
| | | | | | | |  
DB 31 LVVYPWTQRF 40

RESULT 12  
HBBOG  
hemoglobin beta chain - gayal  
C;Species: Bos gaurus frontalis (gayal)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 12-Jul-2004  
C;Accession: A02389  
R;Lalthantluanga, R.; Braunitzer, G.  
Hoppe-Seyler's Z. Physiol. Chem. 365, 737-741, 1984  
A;Title: Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae).  
A;Reference number: A91737; MUID:85005246; PMID:6479895  
A;Accession: A02389

A;Molecule type: protein  
A;Residues: 1-145 <LAL>  
A;Cross-references: UNIPROT:P02071  
C;Superfamily: globin; globin homology  
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
F;2-145/Domain: globin homology <GLB>  
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
| | | | | | | |  
DB 31 LVVYPWTQRF 40

RESULT 13  
HBBOKA  
hemoglobin beta chain - greater kudu  
C;Species: Tragelaphus strepsiceros (greater kudu)  
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 12-Jul-2004  
C;Accession: A02391  
R;Rodewald, K.; Wiesner, H.; Braunitzer, G.  
Biol. Chem. Hoppe-Seyler 366, 395-402, 1985

A;Title: Primary structure of the hemoglobins from the greater Kudu antelope (Tragelaphus  
A;Reference number: A90684; MUID:85279893; PMID:4026993  
A;Accession: A02391

A;Molecule type: protein  
A;Residues: 1-145 <ROD>  
A;Cross-references: UNIPROT:P04245  
A;Note: there are two alleles for the beta chain, one having the sequence shown and the (c  
C;Superfamily: globin; globin homology  
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
F;2-145/Domain: globin homology <GLB>  
F;62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
F;91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
Best Local Similarity 100.0%; Pred. No. 0.0067;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 LVVYPTQRF 10  
 |||||  
 Db 31 LVVYPTQRF 40

## RESULT 14

HDE3  
 hemoglobin beta-III chain - Virginia white-tailed deer  
 C:Species: Odocoileus virginianus virginianus (Virginia white-tailed deer)  
 C:Date: 28-Feb-1985 #sequence\_revision 28-Feb-1985 #text\_change 12-Jul-2004  
 C:Accession: A02393  
 R:Shimizu, K.; Wong, S.C.; Wilson, J.B.; Lam, H.; Reynolds, A.E.; Singh, P.; Huisman, T.  
 Hemoglobin 7, 15-45, 1983  
 A:Title: The primary sequence of the beta chain of Hb type III of the Virginia white-tailed deer hemoglobins, types II, IV, V, and VII, and relationships between intermolecular con  
 A:Reference number: A02393; PMID:83185439; PMID:6841126  
 A:Accession: A02393  
 A:Molecule type: protein  
 A:Residues: 1-145 <SHI>  
 A:Cross-references: UNIPROT:P02074  
 C:Comment: This chain is one of five beta chain alleles.  
 C:Superfamily: globin; globin homology  
 C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
 F:2-145/Domain: globin homology <GLB>  
 F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
 F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10  
 |||||  
 Db 31 LVVYPTQRF 40

## RESULT 15

HBEKN  
 hemoglobin beta chain - European moose  
 C:Species: Alces alces alces (European moose, elk)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 12-Jul-2004  
 C:Accession: A02392  
 R:Aschauer, H.; Wiesner, H.; Braunitzer, G.  
 Hoppe-Seyler's Z. Physiol. Chem. 365, 1323-1330, 1984  
 A:Title: Zur intrinsischen Sauerstoffaffinitaet: die Primaerstruktur eines weiteren Rumi  
 A:Reference number: A91729; PMID:85078042; PMID:6510898  
 A:Accession: A02392  
 A:Molecule type: protein  
 A:Residues: 1-145 <ASC>  
 A:Cross-references: UNIPROT:P02073  
 C:Superfamily: globin; globin homology  
 C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier  
 F:2-145/Domain: globin homology <GLB>  
 F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted  
 F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 58; DB 1; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 0.0067; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10  
 |||||  
 Db 31 LVVYPTQRF 40

Search completed: July 26, 2005, 11:00:29  
 Job time : 39 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 10:42:32 ; Search time 178 Seconds  
(without alignments)  
28.768 Million cell updates/sec

Title: US-09-147-490-1  
Perfect score: 58  
Sequence: 1 LVVYPWTQRF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:\*

1: uniprot\_eprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	17	2 Q9UM85	Q9um85 homo sapien
2	58	100.0	59	2 Q9BXA2	Q9bxa2 homo sapien
3	58	100.0	61	2 Q14484	Q14484 homo sapien
4	58	100.0	61	2 Q14485	Q14485 homo sapien
5	58	100.0	61	2 Q9UBV6	Q9ubv6 homo sapien
6	58	100.0	89	2 Q9UP81	Q9up81 homo sapien
7	58	100.0	101	2 Q14476	Q14476 homo sapien
8	58	100.0	101	2 Q14477	Q14477 homo sapien
9	58	100.0	105	2 Q8IUL9	Q8iul9 homo sapien
10	58	100.0	105	2 Q8IZI0	Q8izi0 homo sapien
11	58	100.0	105	2 Q670S4	Q670s4 homo sapien
12	58	100.0	105	2 Q6J1Z7	Q6j1z7 homo sapien
13	58	100.0	105	2 Q6VOK9	Q6vok9 homo sapien
14	58	100.0	105	2 Q9BMU5	Q9bmw5 homo sapien
15	58	100.0	111	2 Q9BHV6	Q9bhw6 homo sapien
16	58	100.0	113	2 Q02770	Q02770 callithrix
17	58	100.0	115	2 Q9GZL9	Q9gzl9 homo sapien
18	58	100.0	123	2 Q14474	Q14474 homo sapien
19	58	100.0	125	2 Q13072	Q13072 callithrix
20	58	100.0	125	2 Q28799	Q28799 pan troglod
21	58	100.0	128	2 Q9UK54	Q9uk54 homo sapien
22	58	100.0	129	2 Q9UNL6	Q9unl6 homo sapien
23	58	100.0	133	2 Q28552	Q28552 ovis aries
24	58	100.0	141	1 HBBC AMMLE	P68058 ammotragus
25	58	100.0	141	1 HBBC CAPHI	P02078 capra hircu
26	58	100.0	141	1 HBBC OVIMU	P68057 ovis orient
27	58	100.0	141	1 HBBC SHEEP	P68056 ovis aries
28	58	100.0	141	1 HBE CALGE	O13071 callithrix
29	58	100.0	142	2 Q95233	Q95233 perodicticu
30	58	100.0	145	1 HBBA BOSJA	P04346 bos javanic
31	58	100.0	145	1 HBBA CAPHI	P02077 capra hircu

32 58 100.0 145 1 HBBF\_BOVIN  
33 58 100.0 145 1 HBBF\_CAPHI  
34 58 100.0 145 1 HBBF\_SHEEP  
35 58 100.0 145 1 HBB\_ALCAA  
36 58 100.0 145 1 HBB\_BISBO  
37 58 100.0 145 1 HBB\_BOSGF  
38 58 100.0 145 1 HBB\_BOSMU  
39 58 100.0 145 1 HBB\_BOVIN  
40 58 100.0 145 1 HBB\_BUBBU  
41 58 100.0 145 1 HBB\_ODOVI  
42 58 100.0 145 1 HBB\_OVIMU  
43 58 100.0 145 1 HBB\_RANTA  
44 58 100.0 145 1 HBB\_SHEEP  
45 58 100.0 145 1 HBB\_TRAST

#### ALIGNMENTS

#### RESULT 1

Q9UM85 PRELIMINARY; PRT; 17 AA.  
AC Q9UM85;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Beta-globin protein (Fragment).  
GN Name=beta-globin;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96352914; PubMed=8718696;  
RA Rahbar S.; Nozari G.; Forrest G.; Gelbart T.; Forman S.J.; Beutler E.;  
RT "A novel intrachromosomal rearrangement in the beta-globin gene found  
in an African-American family."  
RL Hemoglobin 19:375-388(1995).  
DR EMBL; S82767; AADI4420.1; -.  
DR HSSP; P02023; 1C7C. 17  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 2104 MW; 41977E5BE5260504 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
|||  
DB 2 LVVYPWTQRF 11

#### RESULT 2

Q9BXA2 PRELIMINARY; PRT; 59 AA.  
AC Q9BXA2;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Beta-globin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Kutlar F.; Aguinaga P.M.; Glendenning M.; Kutlar A.;  
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF348448; AAK30154.1; -.  
DR HSSP; P02023; 1DXT.  
DR GO; GO:0005833; C:hemoglobin complex; IEA.  
DR GO; GO:0005344; F:oxygen transporter activity; IEA.

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DR GO; GO:0015671; P:oxygen transport; IEA.
DR PRINTS; PR00814; BETAHAEM.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON TER 59 59
SQ SEQUENCE 59 AA; 6463 MW; 128EF2C12A13A9D3 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 3
Q14484 PRELIMINARY; PRT; 61 AA.
AC Q14484;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-hemoglobin (Beta-globin) (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299720; PubMed=3620470; DOI=10.1016/0167-4781(87)90079-0;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta delta hybrid gene of
hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
exon 2 or between codons 31 and 50."
RL Biochim. Biophys. Acta 909:208-212(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20131369; PubMed=10666717;
RA Fullerton S.M., Bond J.J., Schneider J.A., Hamilton B., Harding R.M.,
RA Boyce A.J., Clegg J.B.;
RT "Polymorphism and divergence in the beta-globin replication origin
initiation region."
RL Mol. Biol. Evol. 17:179-188(2000).
DR EMBL; M25660; AAA53153.1; -
DR EMBL; AF186606; AAF08256.1; -
DR EMBL; AF186608; AAF08260.1; -
DR EMBL; AF186609; AAF08261.1; -
DR EMBL; AF186610; AAF08262.1; -
DR EMBL; AF186611; AAF08263.1; -
DR EMBL; AF186612; AAF08264.1; -
DR EMBL; AF186613; AAF08265.1; -
DR EMBL; AF186615; AAF08267.1; -
DR EMBL; AF186616; AAF08268.1; -
DR EMBL; AF186617; AAF08269.1; -
DR EMBL; AF186618; AAF08270.1; -
DR EMBL; AF186619; AAF08271.1; -
DR EMBL; AF186620; AAF08272.1; -
DR PIR; I52502; I52502.
DR HSSP; P02023; 1DXT.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.

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DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON TER 61 61
SQ SEQUENCE 61 AA; 6691 MW; 905E928EF2C12A13 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 4
Q14485 PRELIMINARY; PRT; 61 AA.
AC Q14485;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-hemoglobin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299720; PubMed=3620470; DOI=10.1016/0167-4781(87)90079-0;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta delta hybrid gene of
hemoglobin P-Nilotic is located within 54 base-pairs of the 5' end of
exon 2 or between codons 31 and 50."
RL Biochim. Biophys. Acta 909:208-212(1987).
RX EMBL; M25661; AAA53154.1; -
DR PIR; I65317; I65317.
DR HSSP; P02023; 1DXT.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON TER 61 61
SQ SEQUENCE 61 AA; 6661 MW; D5DC4F2CC2DDF822 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db 33 LVVYPWTQRF 42

RESULT 5
Q9UBV6 PRELIMINARY; PRT; 61 AA.
AC Q9UBV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-globin (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20131369; PubMed=10666717;  
 RA Fullerton S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,  
 RT "Polymorphism and divergence in the beta-globin replication origin  
 initiation region."  
 RL Mol. Biol. Evol. 17:179-188(2000).  
 DR EMBL; AF186614; AAF08266.1; -;  
 DR EMBL; AF186607; AAF08259.1; -;  
 DR HSSP; P02023; 2HBS.  
 DR GO; GO:0005833; C:hemoglobin complex; IEA.  
 DR GO; GO:0005344; F:oxygen transporter activity; IEA.  
 DR GO; GO:0015671; P:oxygen transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR GO; GO:0002337; Beta haem.  
 DR InterPro; IPR002337; Globin.  
 DR InterPro; IPR000971; Globin.  
 DR Pfam; PF00042; Globin\_1.  
 DR PRINTS; PR00814; BETAHEM.  
 DR PROSITE; PS01033; GLOBIN; 1.  
 DR Heme; Oxygen transport; Transport.  
 KW NON\_TER 61  
 FT SEQUENCE 61 AA; 6661 MW; 304D818EF2C13435 CRC64;  
 SQ  
 Query Match 100.0%; Score 58; DB 2; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 0.012; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;  
 QY 1 LVVYPWTQRF 10  
 DB 33 LVVYPWTQRF 42  
 RESULT 6  
 Q9UP81 PRELIMINARY; PRT; 89 AA.  
 AC Q9UP81  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Mutant beta-globin.  
 GN Name=HBB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99250504; PubMed=10233364;  
 RA Cabeda J.M., Correia C., Estevinho A., Cardoso C., Amorim M.L.,  
 RA Cleto E., Vale L., Coimbra E., Pinho L., Justica B.;  
 RT "Unexpected pattern of beta-globin mutations in beta-thalassemia  
 patients from northern Portugal."  
 RL Br. J. Haematol. 105:168-74(1999).  
 DR EMBL; AF059180; AAD30656.1; -;  
 DR HSSP; P02070; IG08.  
 DR GO; GO:0005833; C:hemoglobin complex; NAS.  
 DR InterPro; IPR002337; Beta haem.  
 DR InterPro; IPR000971; Globin.  
 DR InterPro; IPR009050; Globin\_like.  
 DR Pfam; PF00042; Globin; 1.  
 DR PRINTS; PR00814; BETAHEM.  
 DR PROSITE; PS01033; GLOBIN; 1.  
 DR Heme; Oxygen transport; Transport.  
 KW SEQUENCE 89 AA; 9689 MW; 4A1389288BEEF0D1 CRC64;  
 SQ  
 Query Match 100.0%; Score 58; DB 2; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10  
 DB 33 LVVYPWTQRF 42  
 RESULT 7  
 Q14476 PRELIMINARY; PRT; 101 AA.  
 ID Q14476  
 AC Q14476  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE G-gamma-hemoglobin gene from Greek HPFH mutant, complete cds.  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86017015; PubMed=2413469;  
 RA Gelinas R., Yagi M., Endlich B., Lotshaw C., Kazazian H.H.Jr. .,  
 RA Stamatoiyannopoulos G.;  
 RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma)  
 HPFH mutant: evidence for a distal CCAAT box mutation in the A-gamma  
 gene."  
 RL Prog. Clin. Biol. Res. 191:125-139(1985).  
 DR EMBL; M32723; AAA35955.1; -;  
 DR HSSP; P01922; 1FDH.  
 DR GO; GO:0005833; C:hemoglobin complex; IEA.  
 DR GO; GO:0005344; F:oxygen transporter activity; IEA.  
 DR GO; GO:0015671; P:oxygen transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR002337; Beta haem.  
 DR InterPro; IPR000971; Globin.  
 DR InterPro; IPR009050; Globin\_like.  
 DR Pfam; PF00042; Globin; 1.  
 DR PRINTS; PR00814; BETAHEM.  
 DR PROSITE; PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transport.  
 FT NON\_TER 101  
 SQ SEQUENCE 101 AA; 11039 MW; 8489D25BBDE29BA5 CRC64;  
 Query Match 100.0%; Score 58; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LVVYPWTQRF 10  
 DB 33 LVVYPWTQRF 42  
 RESULT 8  
 Q14477 PRELIMINARY; PRT; 101 AA.  
 ID Q14477  
 AC Q14477  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE HBB protein (fragment).  
 GN Name=HBB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84178511; PubMed=6324786;  
 RA Kimura A., Ohta Y., Fukumaki Y., Takagi Y.;  
 RT "A fusion gene in man: DNA sequence analysis of the abnormal globin  
 gene of hemoglobin Miyada."  
 RL Biochem. Biophys. Res. Commun. 119:968-974(1984).  
 DR EMBL; K01899; AAA52635.1; -;

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DR HSSP; P02023; 1DXT.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport.
FT NON TER 101
SQ SEQUENCE 101 AA; 10928 MW; F54BFD8224B5DB0F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db |||||
33 LVVYPWTQRF 42

RESULT 9
ID Q8IUL9 PRELIMINARY; PRT; 105 AA.
AC Q8IUL9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemoglobin beta chain variant Hb.Sinai-Bel Air (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole blood;
RA Kutlar F., Holley L., Elam D., Dutton C., Dainer E.M., Kutlar A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540397; AANI16468.1; -.
DR HSSP; P02023; 1DXT.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport.
FT NON TER 105
SQ SEQUENCE 105 AA; 11548 MW; F03ABCF853A4FFP CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db |||||
33 LVVYPWTQRF 42

RESULT 10
Q8IZIO PRELIMINARY; PRT; 105 AA.
ID Q8IZIO
AC Q8IZIO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemoglobin beta chain variant Hb-I_Toulouse (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dainer E.M., Kutlar F., Holley L., Glendenning M., Kutlar A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136511; AANI1321.1; -.
DR HSSP; P02023; 1DXT.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport.
FT NON TER 105
SQ SEQUENCE 105 AA; 11505 MW; 26ECBC9588C9AED CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db |||||
33 LVVYPWTQRF 42

RESULT 11
Q670S4 PRELIMINARY; PRT; 105 AA.
ID Q670S4
AC Q670S4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hemoglobin Lepore-Baltimore (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole blood;
RA McKeown M., Holley L., Nechtman J., Kutlar F.;
RT "Molecular characterization of African-American chromosome carrying
the Hb Lepore-Baltimore (delta68Leu/beta 84Thr) gene identified by PCR
amplified sequencing."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY695366; AAU08171.1; -.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport.
FT NON TER 105
SQ SEQUENCE 105 AA; 11459 MW; FADD4606FAA4F614 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10
Db |||||

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Db          33 LVVYPWTQRF 42

RESULT 12
Q6J1Z7      PRELIMINARY;      PRT;      105 AA.
AC Q6J1Z7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hemoglobin beta (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Atalay E.O., Elam D., Nechtman J., Kutlar A., Kutlar F.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY605052; AAT3651.1; -.
DR HSSP; P02023; IBA8.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 105
SQ SEQUENCE 105 AA; 11446 MW; 443ABBA3F54BF8E2 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db          33 LVVYPWTQRF 42

RESULT 13
Q6V0K9      PRELIMINARY;      PRT;      105 AA.
AC Q6V0K9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Mutant hemoglobin beta chain (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Kutlar F., Mirmow D., Glendenning M., Kutlar A.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY356351; AAA63175.1; -.
DR HSSP; P02023; IBA8.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db          33 LVVYPWTQRF 42

RESULT 14
Q9BWU5      PRELIMINARY;      PRT;      105 AA.
AC Q9BWU5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Mutant hemoglobin beta chain (Fragment).
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Kutlar F., Leithner C., Briscoe J., Kutlar A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY027800; AAK1581.1; -.
DR HSSP; P02023; 2HBS.
DR GO; GO:0005833; C:hemoglobin complex; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002337; Beta haem.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 105
SQ SEQUENCE 105 AA; 11501 MW; 8143C84D90C01687 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db          33 LVVYPWTQRF 42

RESULT 15
Q9BWV6      PRELIMINARY;      PRT;      111 AA.
AC Q9BWV6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mutant beta globin.
GN Name=HBB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.  
RC TISSUE=Whole blood;  
RA Kutlar F., Adekunle A.D., Leithner C., Kutlar A.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY027509; AAK20080.1; -.  
DR HSSP; P02023; 1DXT.  
DR GO; GO:0005833; C:hemoglobin complex; IEA.  
DR GO; GO:0005344; F:oxygen transporter activity; IEA.  
DR GO; GO:0015671; P:oxygen transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002337; Beta\_haem.  
DR InterPro; IPR000971; Globin.  
DR InterPro; IPR009050; Globin\_like.  
DR Pfam; PF00042; Globin; 1.  
DR PRINTS; PR00814; BETAHAEM.  
DR PROSITE; PS01033; GLOBIN; 1.  
KW Heme; Oxygen transport; Transport.  
SQ SEQUENCE 111 AA; 12234 MW; 8992F924B5B3903A CRC64;

Query Match 100.0%; Score 58; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVVYPWTQRF 10  
| | | | |  
Db 33 LVVYPWTQRF 42

Search completed: July 26, 2005, 10:56:54  
Job time : 179 secs